STIC-Biotech/ChemLib

From: Sent:

Ibrahim, Medina A. Programmer 18, 2002 6:49 PM RECEIVED STIC-Biotech/ChemLib 09/538, 396

To: Subject:

Please search the following:

. ICA/CHEM. D. VISICA (ST.C)

1.oligo search of at least 30 contiguous bases of SEQ ID NO:1.2. residue of at least 20 contiguous amino acids of SEQ ID NO:2. Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9A12 (703)306-5822

> · Sale of Granact: Toby Pust

rechnical info. Specialist CM1 6A04 703-308-3534

Searcher:
Phone:
Location:
Date Picked Up: ルカロ
Date Completed: Taple
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Total number of hits satisfying chosen parameters: Title: Perfect score: Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Word size : Searched: Run on: OM nucleic - nucleic search, using sw model Post-processing: Listing first 1000 summaries Scoring table: Sequence: No matches found Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Query Score Match Length DB Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

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4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:* US-09-538-396-1 OLIGO_NUC Gapop 60.0 , Gapext 60.0 December 26, 2002, 05:24:41; Search time 125 Seconds (without alignments) 14598.440 Million cell updates/sec 363474 segs, 203117208 residues 1 aattcggcacgagtggatcc.....atctagcatcaaaaaaaaa 4492 ID SUMMARIES 0 Description

Result No.

Search completed: December 26, 2002, 08:43:45 Job time: 127 secs

OM protein - protein search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

December 26, 2002, 08:43:51; Search time 27 Seconds

(without alignments)
1434.095 Million cell updates/sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5965427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                  TELEFAX: (415) 324-09 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 324-09 INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                 REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Chall Challon
                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PATENTIA RELEASE #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Human R
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                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 17-JUL-1996
TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                   NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                  ENGTH:
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Pred. No. 4.8e-20;
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Minimum Maximum

DB seq

length: 0 length: 2000000000

Total number of hits'satisfying chosen parameters:

N

0;

Word size : Searched:

20

Scoring table: Sequence: Perfect score: Title:

OLIGO

Gapext 60.0 29422922 residues

262574 seqs, Gapop 60.0 , US-09-538-396-2
1316
1 MSTVDKMLIKGIRSFDPDNK.....YRVSKDENQHSIIESQEIFD 1316

Database :

Post-processing: Listing first 1000 summaries

Issued_Patents_AA: *

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US-08-592-126-148

Sequence 148, Application US/08592126 Patent No. 5821091

Patent No. 5821091
GENERAL INFORMATION:

APPLICANT: Gregory Dolganov TITLE OF INVENTION: Transcr TITLE OF INVENTION: Polypep

Transcripts Encoding Immunomodulatory Polypeptides

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates

CITY: Palo Alto STATE: CA

STREET:

350 Cambridge

Avenue,

Suite 250

COUNTRY:

USA

94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

E: Floppy disk IBM PC compati

compatible PC-DOS/MS-DOS

OPERATING SYSTEM:

Result

score greater than or equal to the score or נהפי ויישיא and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

/cgn2_6/ptodata/1/iaa/backfiles1.pep:*

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Score

Match

Length DB $\frac{1312}{1312}$

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Description

Sequence 148, App Sequence 51, Appl 148,

US-08-592-126-148 US-08-687-080-51

ALIGNMENTS

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Result
No.
Search completed: December 26, 2002, 08:52:12 Job time : 39 secs
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Perfect score:
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                       Description
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A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84727
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1292 <STO>
A:Cross references: GB:AE002093; NID:g4263721; PIDN:AAD15407.1; GSPDB:GN00139
C:Genetics:
                                                                                                                                                                                                                                             probable RAD50 DNA repair protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002 C;Accession: D84727 R;Accession: D84727 R;Accession: D84727 R;Din, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Gene: At2g31970
A;Map position: 2
C;Superfamily: RAD50 protein
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pir2:*
pir3:*
pir4:*
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(c) 1993 - 2002
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Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable RAD50 DNA probable DNA repai
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probable DNA repair protein RAD50 - mouse C:Species: Mus musculus (house mouse) C:Species: Mus musculus (house mouse) C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Mar-2000 C:Accession: T30845 R:Kim, K.K.; Daud, A.I.; Wong, S.C.; Pajak, L.; Tsai, S.C.; Wang, H.; Henzel, W.J.; F. J. Biol. Chem. 271, 29255-29264, 1996 A;Fitle: Mouse RAD50 has limited epitopic homology to p53 and is expressed in the adu A;Reference number: Z20899; MUID:97067183; PMID:8910585 A;Accession: T30845 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                              δõ
                                                                                                                                                                                                                          A; Map position: 11
C; Superfamily: RAD50 protein
C; Keywords: DNA repair
                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U66887; NID:g1575574; PID:g1575575; PIDN:AAC52894.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
T30845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
Search completed: December 26, Job time: 46 secs
                                                                            맑
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1312 <KIM>
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                                                                                                                                                                                                                                                                                     A;Gene: RAD50
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                                                                                                                                                     Matches
                                                                                                                                                                      Best
                                                                                                                                                                                        Query Match
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                                                                                            1207 MRGRCSAGQKVLASLIIRLALAETFCLNCGILALDEPTTNLD 1248
                                                                        1197 MRGRCSAGQKVLASLIIRLALAETFCLNCGILALDEPTTNLD 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 LENVIFVHQDESNWPLQDPSTLKKKFDDIFSATRYTKALEVIKKLHKDQ 200
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                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.7%;
                                                                                                                                                                     3.2%;
                 2002, 08:50:24
                                                                                                                                                                     Score 42;
; Pred. No.
                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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Pred. No.
                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; L
6.6e-40;
                                                                                                                                                                     DB 2; L; 7.2e-33;
                                                                                                                                                   0;
                                                                                                                                                                                      Length 1312;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 26, 2002, 07:47:17; Search time 25 Seconds (without alignments) 2183.314 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-538-396-2 1316 1 MSTVDKMLIKGIRSFDPDNK.....YRVSKDENQHSIIESQEIFD 1316

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 20

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Query Score Match Length DB SUMMARIES

IJ

Description

No matches found

Search completed: December 26, 2002, 08:47:34 Job time: 25 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2002, 05:15:21; Search time 104 Seconds (without alignments) 13246.077 Million cell updates/sec

US-09-538-396-1 4492

Title: Perfect score: Sequence: 1 aattcggcacgagtggatcc.....atctagcatcaaaaaaaaa 4492

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Scoring table:

Searched: 441362 seqs, 153338381 residues

Word size : 30

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB Ħ Description

No matches found

Search completed: December 26, 2002, 08:41:16 Job time: 105 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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                                                                                                                                                                                                                                                                     ENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   TUMBER OF SEQUENCES:
                                                                                                                                         STREET:
                                                                                      COUNTRY:
                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                 LE OF INVENTION:
                                                                                                                                                                                                                  LE OF INVENTION:
                                                                                                                        ITY: Palo Alto
                                                                                                                                                                                                                                                                                          No.
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                                                                       94306
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Gapop 60.0 ,
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1316
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                                                                                                                                                                                                                                                                                                         Application US/08592126
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                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                              Dehlinger & Associates
                                                                                                                                           Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1312
1312
compatible
PC-DOS/MS-DOS
                                                                                                                                                                                                   Polypeptides
151
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_6/ptodata/1/1aa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                     ranscripts Encoding Immunomodulatory
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(without alignments)
1434.095 Million cell updates/sec
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US-08-687-080-51
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                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 148, App
Sequence 51, Appl
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; INDIVIDUAL ISOLATE: US-08-592-126-148
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LENGTH: 1312 amin Type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100. Matches \bigwedge 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51,
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PATENTIN Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HENT NO. 5965427
                                                                                            TELEFAX: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1197
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                              REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                        APPLICATION NUMBER: US 0
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT Charleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Camb
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IOPOLOGY:
                              STRANDEDNESS:
                 TOPOLOGY:
                                                                                                                                                                              REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRGRCSAGQKVLASLIIRLALAETFCLNCGI 12:
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                                                                                                                                                                                             Sholtz, Charles
                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08687080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                               (415) 324-0960
OR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregory Dolganov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version
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                 linear
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                           single
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Pred. No.
                                                                                                                                                                4600-0111.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8e-20
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; HYPOTHETICAL: NO
; ANYI-SENSE: NO
ORIGINAL SOURCE;
INDIVIDUAL ISOLATE: TRANS. OF RAD50 cDNA (SEQ. 54), NT.
INDIVIDUAL ISOLATE: 389 TO 4324
US-08-687-080-51
Query Match
Best Local Similarity 100.0%; Pred. No. 4.8e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1207 MRGRCSAGQKVLASLIIRLALAETFCLNCGI 237
Db 1197 MRGRCSAGGKVLASLIIRLALAETFCLNCGI 1227
Search completed: December 26, 2002, 08:51:12
Job time: 27 secs
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OM nucleic -
RESULT 1
AAC66915
ID AAC6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 1000 summaries
                                                                                                                                                                                                                               Result
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding Rad50 production and for producing gene expression -
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P-PSDB; AAB27248.
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2640	GAGAAAAACTTGAATCAACATTTGGCGGATGAAAGTCAGAAGGCGCAGGCCATTTGATGAT	2581	Qy
2580	AAACTTCGGACTATCTATGATGCTTATGTGAAGCTGGTAGAAGAAAACCATACCTCTAGCA	2521	Db
2580	CTTCGGACTATCTATGATGCTATGTGAAGCTGGTAGAAGAAACCATACCTCTAC	S	Ωу
2520	TCTAAAGCTCTGGCAATGGAATCATCAAATGCTGAAGCTCTTTTTCAGCAATTGG		Дb
2520	AGATCTAAAGCTCTGGCAATGGAATCATCAAATGCTGAAGCTCTTTTTCAGCAATTGGAT	4	Qy
2460	TCAAGTACT	2401	Δb
2460	CTGATGAGGAGGATGAGTTCGTGAAGAAACAAAGGATGCAAAACTCAAGTACT	4	Qy
2400	GAACGTGCTTTCAC	2341	. Db
2400	CTTTTGAACATTTGGCTCGGAAGAATCATGTATGCCCATGCTGT	2341	Qy
2340	AAAGAGATGAACAGAAAAGATTAGAGAATTTCGCAAATGGAATGCGGGAAATGCTTGCA	2281	Дb
2340	HGATGAACAGAAAAGATTAGAGAATTCGCAAATGGAATGCGGGAAATGCTTGC	2281	Qy
2280	ATTTACAGATATCTGCTAATGTTGACATGTTTCCCAAAGTTCTACAAGACGCCATGAAC	2221	ДD
2280	ACAGATATCTGCTAATGTTGACATGTTTCCCCAAAGTTCTACAAGACGCCCATG	2221	Qγ
2220	TCCTGGACTCGAAACTTCAATC		DЬ
2220	CAAAACTTCGAAGAGATATGGATG	2161	Qy
2160	TAACTGATGCTAGAGAACAATT	2101	Db
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2100	ACAAGGAATACAATGAGTTAAGATCAAAATCCCA	2041	Db
2100	TCAAGCCTTTTGGCCTGTGG	2041	Оу
2040	TACTTAGGGGGAGGAATCCTTTTGAGAAGGATATGAAGAAGGA	1981	Db
2040	ATAAAATCAAAAAGGTACTTAGGGGGAGGAA	1981	Qy
1980	GACAAGCTCAATGAGATAGTTAATGAGCATAA	1921	Дb
1980	AAGGATGCATTGGAAAGCAGCAAGGACAAGCTCAATGAGATAGTTAAT	192í	Qy
1920	AAAGATATAATAAATAGAAATGCTGATGAAAGAGTAAAACTGGGTTT	1861	Db
1920	TTCTGCGGGAGAAAGATATAATAAATAGAAATGCTGATGAAAAGAGTAAAACTGGG	1861	Qy
1860	agtcagaaacgaacagaagtatatagtttggaacagaaaataaaagt	1801	DЬ
1860	ATTCAATTATAAGTCAGAAACGAACAGAAGTATATAGTT	1801	Qy
1800	GAGAGACATATGCAAATTGAAGTCGAGAGGAAGACACTTGCGCTTGGAGAAAGAGACTAT	1741	Db
1800	AGAGACATATGCAAATTGAAGTCGAGAGGAAGACACTTGCGCTTGGAGAAAGAGAC	74	Qy
1740	GAACGCGATGCTGCAGAAGTGGAGCTTTCAAAATTTAATCTATCCCGTATCGATGAGAGG	1681	Дb
1740	AACGCGATGCTGCAGAAGTTGGAGCTTTCAAAATTTTAATCTATCCCGGTATCGATGAGAG	O.	Qy
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1680	RCAATCTAAGATTGAATCCATGTCAGGCATTTTAAGACGGAGAAAA	1621	Оу
1620	GATGTTTTGTGGAAACACTATCTTAAAATAAATGCTCGCTACTCCGAAGTTGATGGTCAG	CD .	DЬ
1620	atgitttgtggaaacactaicttaaaataaatgctcgctactccgaagttgatggi	ĊΠ	Qy
1560	TATCAAGTCTTGAGAATGATTTGCTGGATAAGAAGAAATCCAATGAAGATCAGTT	1501	В
1560	ACTATCAAGTCTTGAGAATGATTTGCTGGATAAGAAGAAATC	1501	Qy

3720	61 CTCCAGCTTAAGACAACTGAAATGGCAAACAAGGACTTGGACAGATATTATACTGCTTTA	360	Qγ
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3540 3540	31 AGCTTGTCTGCTATAGAAGCTGATCTGAAACGCCATTCTCAAGAAAAAAGAGAGGCTTAAT 		g 04
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3360 3360)1 TGCATGGCAAAACAGCAAAGAATATCAGCTGAGTTAAACAAGAGCAAAGAACTACTGCAG 	w w	g Qy
3300 3300	1 AACGAAAAGCTTAAGGAATTGCAGGGAAGGCATGTTCTTTGCCATTCTCAGTTACAGAGT	324 324	д 9
3240 3240	11 GAACTTGATGCTCTTGGAAGACTTAATATGAAGATAAAAGGGTACTTGGATTCCAAGAAA 		DP QA
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BE443510

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4041 Forest Park Ave, 9
Tel: 314 615 6979
Fax: 314 615 5975
                                                         sequence.
BG649394
BG649394.1
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GeneThresher methylation
Unpublished (2002)
Contact: Bedell JA
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Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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Class: shotgun
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Plate: fzmb013f006 row: d colu
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      sorghum
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/dlone="fzmb013f00607"
/clone="fzmb013f00607"
/clone="organ: flatered library"
/clone="organ: leaf; Vector: pBCSK('); Site_1: HincII; DNA
/note="organ: leaf; Vector: pB
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/cultivar-"MO17"
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100.0%; Pred. No. 1.3e-52;
Live 0; Mismatches 0;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
Contact: Cordonnier-Pratt My
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and An EST database from Sorghum: developing embryos Unpublished (2000)
                                                                                                                                               1 (bases 1 to 484)
Reid, FP., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.
An EST database from Sorghum: developing embryos
Unpublished (2000)
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 25 hr; Site of 25 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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6.5e-37;
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Best Local
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                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATGA 4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mmpratteuga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
15 20. Three-prime sequences, which are obtained with PolyTMix or
T7 sequencing primer, are presented as the reverse complement.
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIC1_50_G12.g1_A002 Pathogen-infected bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
                                                                                                                                                                                 Seq primer:
High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An EST database from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C., Sudman, M. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                       POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 706 583 0210
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                                                                                                                                                                             quality sequence stop: 308
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/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector: Xho; Site_1: Xho
   /organism="Sorghum bicolor"
/cultivar="BTx623"
                                                                                                             Location/Qualifiers
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/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum: plants infected with a compatible
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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3.1e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NA linear EST 04-JAN-2002 compatible 1 (PIC1) Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 484;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 GGTCAAAGGCAGCTTGCTGAGAAGTACTATCGAGTCTCCAAGGATGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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Lotus japonicus

Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papillonoideae; Loteae;

Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Freund,S., Stougaard,J. and Udvardi,M. Lotus japonicus root nodule ESTs: a tool for functional genomics Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Udvardi MK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI416347.1 GI:15186602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nodules Lotus japonicus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINEST2d3r Lotus japonicus nodule library, mature and immature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: udvardi@mpimp-golm.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: T7
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                                                       178
                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 549.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site_1: xhoI; Site_2: ECORI; Four-week-old sorghum seedlings were sprayed with spore suspension prepared from 3-week-old FRM421, a sorghum isolate of the anthracnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colletotrichum graminicola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Pathogen-infected compatible 1 (PIC1)"
/tissue_type="Leaves"
                                                                                                          ECORI; Site_2: XhoI; The library was prepared using mRNA extracted from a mixture of mature (pink) and immature (white) nodules of Lotus japonicus ecotype 'Gifu'. Nodule (white) nodules of Lotus japonicus ecotype 'Gifu'. Nodule (white) nodules of Lotus japonicus ecotype 'Gifu'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript II SK(-) from Lambda Zap
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                                                                                                                                                                                                                                                                                                                                      /cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
                                                                                                                                                                                                                                            /note="Organ: Nodule; Vector: pBluescript SK-; Site_1:
                                                                                                                                                                                                                                                                      /clone_lib="Lotus japonicus nodule library, mature and
immature nodules"
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Lotus japonicus"
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Pred. No.
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                                                                                                                              ORIGIN
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                                                             Query Match
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RESULT 5 BI416347

DEFINITION

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ACCESSION VERSION

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ORGANISM

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COMMENT

BASE COUNT

0.7%; Score 30; DB 10; ilarity 100.0%; Pred. No. 0.0047; Conservative 0; Mismatches 0

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RESULT 6
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE443510 458 bp mRNA linear EST 25 WHEII15_D09_H17ZS Wheat etiolated seedling root normalized library Triticum aestivum cDNA clone WHEII15_D09_H17, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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                                                                                                                                                                                                                                                                            surface-sterilized, germinated and grown assptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystalization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Featon) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before
excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. col1 DH10B"
/note="Vector: Lambda Un1-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1115_D09_H17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev_stage="Five day old etiolated seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'tissue_type-"Root"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative RAD50 DNA repair protein (DNA repair-recombination
                                                                                                                InterPro; IPR001395; AHC_trans
InterPro; IPR004584; Rad50.
TIGRFAMS; TIGR00606; rad50; 1.
PROSITE; PS00063; ALDOKETO
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Eukaryota; Viriddiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                              MEDIJINE-20386653; pubMed-10908350;
Lanson N.A. Jr., Egeland D.B., Royals B.A., Claycol
Tanson N.A. Jr., Egeland D.B., Royals B.A., Claycol
The MRE11-NB51-RAD50 pathway is perturbed in SV40
immortalized AT-1, AT-2 and HI-1 cardiomyocytes.";
Nuclaic Acida Res. 28:2882-2892(2000).
EMBL; AF218576; AAF91229.1;
EMBL; AF218576; AAF91229.1;
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001395; Aldo/ket_red.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disruption of the Arabidopsis RAD50 gene leads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 LENVIFVHQDESNWPLQDPSTLKKKFDDIFSATRYTKALEVIKKLHKDQ 200
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 LENVIFVHQDESNWPLQDPSTLKKKFDDIFSATRYTKALEVIKKLHKDQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. 25:31-41(2001).
AC006223; AAD15407.2;
AF168748; AAF36810.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                     PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1
1312 AA; 153783 MW; F13C041BD2C05932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR00606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR004584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 (TrEMBLrel. 15,
0 (TrEMBLrel. 15,
2 (TrEMBLrel. 21,
3.2%;
nilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Last sequence update)
Last annotation update)
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Pred. No.
       Score 42; DB 11;
; Pred. No. 5.3e-32;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89DC4F6BCA39B0E8 CRC64;
                                                                                                        F13C041BD2C05932 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bouchez D., Bechtold N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                Claycomb
                                                         Length 1312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to plant sterility and
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RESULT 4
OPUP86

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P70388;
01-FEB-1997
01-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003439; ABC_transportr.
InterPro; IPR001395; Aldo/Ket_red.
InterPro; IPR004584; Rad50.
TIGR7AMS; TIGR00606; rad50; 1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_SEQUENCE 1312 AA; 153487 MW; 4AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJIE-97067183; PubMed-8910585;
Kim K.K., Daud A.I., Wong S.C., Pajak L., T
Henzel W.J., Field L.J.;
"Mouse RAD50 has limited epitopic homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99346140; PubMed-10415333;
MEDLINE-99346140; PubMed-10415333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAD50 OR RAD50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:109292; Rad50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
                                                                    InterPro; IPR003439; ABC_transportr.
InterPro; IPR0043195; Aldo,ket_red.
InterPro; IPR004584; Rad50.
TIGRPAMS; TIGR00606; rad50; 1.
                                                                                                                                                                                                       Gene 235:59-67(1999).
EMBL; AF057300; AAD50326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated RAD50 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98406
                                                                                                                                                                                                                                                                            RAD50
                                                                                                                                                                                                                                                                     Molecular cloning and characterization of splice variants of ADSO gene. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult myocardium. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRGRCSAGQKVLASLIIRLALAETFCLNCGILALDEPTTNLD 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRGRCSAGQKVLASLIIRLALAETFCLNCGILALDEPTTNLD 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U66887; AAC52894.1; -.
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42; Conserv
                                     PS00063;
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|etazoa; Chordata;
|theria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
          A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALDOKETO_REDUCTASE_3; UNKNOWN_1.
A; 153487 MW; 4AF9AF9AD9E1D7A2 CRC64;
      ALDOKETO_REDUCTASE_3; UNKNOWN_1.
A; 138432 MW; D6734A4E4D898AAE CRC64;
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Last sequence update)
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Last sequence update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                            Kim P.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
5.3e-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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                                                                                                                                                                                                                                                                                                                                                                            Koh J.T., Kim J.H.,
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RESULT 5
Q92878
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043254
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Best Local Similarity
Matches 31; Conserv
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Best Local
                                                                                                                                                                                                                                                                               Matches
                                                                                                                        043254 PRELIMINARY;
043254;
01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
RAD50 homologue hsRAD50.
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Q92878;
Q9-7EB-1997
Q1-FEB-1997
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                                                                                                                                                                                                                                                                                                                       Gene 235:59-67(1999).

Gene 235:59-67(1999).

EMBL; 063139; AAB07119.1; -

EMBL; AF057299; AAD50325.1;

InterPro; IPR003439; ABC_transportr.

InterPro; IPR001395; Aldo/ket_red.

InterPro; IPR004584; Rad50.

TIGREPRO; IRR004584; Rad50; 1.

PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.

SEQUENCE 1312 AA; 153891 MW; 1F208C3817FC41FC 0
TISSUE-TESTIS;
Offenberg H.H.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; Z75311; CAA99729.1; -.
                                                                      AAD-7.
RAD50.
Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                              1207 MRGRCSAGQKVLASLIIRLALAETFCLNCGI 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99346140; PubMed=10415333;
Shin B.A., Seo K.H., Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                    1197 MRGRCSAGQKVLASLIIRLALAETFCLNCGI 1227
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Dolganov G.M., Maser R.S., Novikov
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                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        RAD50
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                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                          Similarity
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Pred. No.
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DR InterPro; IPR003439; ABC_transportr.

DR InterPro; IPR001395; Aldo/Ret_red.

DR InterPro; IPR004584; Rad50;
DR TIGRFAMS; TIGR00506; rad50; 1.

DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.

SQ SEQUENCE 1318 AA; 154410 MW; B4EB9EEEB8105822 CRC64;

SQ SEQUENCE 1318 AA; 154410 MW; B4EB9EEB8105822 CRC64;

SQ SEQUENCE 1318 AA; 154410 MW; B4EB9EEB8105822 CRC64;

SEQUENCE 1318 AA; 154410 MW; B4EB9EEEB8105822 CRC64;

SEQUENCE 1318 AA; 154410 MW; B4EB9EEB8105822 CRC64;

SEQUENCE 1318 AA; 154410 MW; B4EB9EEB810582 CRC64;

SEQUENCE 1318 AA
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Copyright (c) 1993 - 2002 Compugen
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Matches 1316; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding Rad50 polypeptides, useful for transgenic plant production and for producing antibodies that are useful for modifying gene expression -
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N-PSDB; AAC66915.
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                                                                                                                                        RIMEARKGQENFQLIVITHDERFAHLIGQRQLAEKYYRVSKDENQHSIIESQEIFD
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RAD50
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RESULT 3
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Query Match
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Matches 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; RAD50; DNA repair; tumour suppression; cancer; Septin-2;
central nervous system.
                                                                                                                                                                                                                                                                                                                                     Human tumour suppressor gene RAD50 - useful to detect predisposition to, decrease risk of and treat cancer, also Septin-2 homologues \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1996;
26-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 82-86; 195pp;
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N-PSDB; AAT75237.
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                                                                                                                                                                                              Human homologue of yeast RAD50.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                        Human homologue;
                                                                                                                                                                                                                        25-NOV-1998
                                                                                                                                                                                                                                                  AAW71295
                                                                                                                                                                                                                                                                          AAW71295 standard; Protein;
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                                                         27-FEB-1997;
                                                                                   03-SEP-1998
                                                                                                           WO9838306-A1
                                                                                                                                   Homo sapiens
                                                                                                                                                            Lmmunomodulatory
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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96US-0592126.
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                                                          97WO-US03159
                                                                                                                                                            yeast RAD50; Drosophila Septin-2; activity; identification; activate
                                                                                                                                                                                                                                                                                                                                                                                                     2.4%;
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Pred. No.
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5.7e-21;
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Dolganov G;

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Search completed: December 26, 2002, 08:45:17 Job time : 70 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human homologue of the yeast S. cerevisiae gene RAD50. The present sequence has 38 overall homology to the yeast RAD50 gene, and is expressed in activated T-cells, testis, foetal liver and heart tissues. The specification also describes sequences encoding human homologues of the yeast RAD50, the Drosophila Septin-2 and Acyl-CoA synthetase. The proteins have immunomodulatory activity. The nucleic acids and proteins can be used to identify activated T-cells in a sample population. They can also be used to isolate and identify sequences encoding other proteins or other compounds having immunomodulatory
                                                                                                                                1197 MRGRCSAGQKVLASLIIRLALAETFCLNCGI 1227
                                                                                                                                                                                                 1207 MRGRCSAGQKVLASLIIRLALAETFCLNCGI 1237
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Pages 136-140; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human immunomodulatory poly:peptide(s) - have homology to the yeast RAD50 or Drosophila Septin-2 proteins
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N-PSDB; AAV59979.
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1 AATTCGGCACGAGTGGATCCATTAGCACCCATAGCCGTACAAAACCCTAAGAACCCTAAC 60

Query Match 100.0%; Score 4492; Best Local Similarity 100.0%; Pred. No. 0; Matches 4492; Conservative 0; Mismatches

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Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone;Oyla88_D09.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidese; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced
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The nucleotide sequence of this BAC clone was generated by
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be reserved.
  Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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